

M:
Belyavskyi



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/658,621B

DATE: 04/30/2003

TIME: 13:04:21

Input Set : A:\02-11-14 029395-017.ST25.txt

Output Set: N:\CRF4\04302003\I658621B.raw

3 <110> APPLICANT: Taylor-Papadimitriou, Joyce
4 Heukamp, Lukas Carl
5 Offringa, Rienk
6 Melief, Cornelis Johanna Maria
7 Acres, Bruce
8 Thomas, Mireille
10 <120> TITLE OF INVENTION: MUC-1 derived peptides
12 <130> FILE REFERENCE: 029395-017
14 <140> CURRENT APPLICATION NUMBER: US 09/658,621B
15 <141> CURRENT FILING DATE: 2000-09-08
17 <150> PRIOR APPLICATION NUMBER: US 60/187,215
18 <151> PRIOR FILING DATE: 2000-03-03
20 <150> PRIOR APPLICATION NUMBER: GB 9921242.5
21 <151> PRIOR FILING DATE: 1999-09-08
23 <150> PRIOR APPLICATION NUMBER: EP 99 40 2237.4
24 <151> PRIOR FILING DATE: 1999-09-10
26 <160> NUMBER OF SEQ ID NOS: 80
28 <170> SOFTWARE: PatentIn version 3.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1572
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (58)..(1542)
39 <400> SEQUENCE: 1

ENTERED

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| 42 | atg aca ccg ggc acc cag tct cct ttc ttc ctg ctg ctg ctc ctc aca | 105 |
| 43 | Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr | |
| 44 | 1 5 10 15 | |
| 46 | gtg ctt aca gtt gtt aca ggt tct ggt cat gca agc tct acc cca ggt | 153 |
| 47 | Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly | |
| 48 | 20 25 30 | |
| 50 | gga gaa aag gag act tcg gct acc cag aga agt tca gtg ccc agc tct | 201 |
| 51 | Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser | |
| 52 | 35 40 45 | |
| 54 | act gag aag aat gct gtg agt atg acc agc agc gta ctc tcc agc cac | 249 |
| 55 | Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His | |
| 56 | 50 55 60 | |
| 58 | agc ccc ggt tca ggc tcc tcc acc act cag gga cag gat gtc act ctg | 297 |
| 59 | Ser Pro Gly Ser Gly Ser Thr Thr Gln Gly Gln Asp Val Thr Leu | |
| 60 | 65 70 75 80 | |
| 62 | gcc ccg gcc acg gaa cca gct tca ggt tca gct gcc acc tgg gga cag | 345 |

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63 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
64      85      90      95
66 gat gtc acc tcg gtc cca gtc acc agg cca gcc ctg ggc tcc acc acc      393
67 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
68      100      105      110
70 ccg cca gcc cac gat gtc acc tca gcc ccg gac aac aag cca gcc ccg      441
71 Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
72      115      120      125
74 ggc tcc acc gcc ccc ccg gcc cac ggt gtc acc tcg gcc ccg gac acc      489
75 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
76      130      135      140
78 agg ccg ccc ccg ggc tcc acc gcc ccc gcc gcc cac ggt gtc acc tcg      537
79 Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His Gly Val Thr Ser
80 145      150      155      160
82 gcc ccg gac acc agg ccg gcc ccg ggc tcc acc gcc ccc ccg gcc cac      585
83 Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
84      165      170      175
86 ggt gtc acc tcg gcc ccg gac aac agg ccg gcc ttg ggc tcc acc gcc      633
87 Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala
88      180      185      190
90 cct cca gtc cac aat gtc acc tcg gcc tca ggc tct gca tca ggc tca      681
91 Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser
92      195      200      205
94 gct tct act ctg gtg cac aac ggc acc tct gcc agg gct acc aca acc      729
95 Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr
96      210      215      220
98 cca gcc agc aag agc act cca ccc agc att ccc agc cac cac tct gat      777
99 Pro Ala Ser Lys Ser Thr Pro Pro Ser Ile Pro Ser His His Ser Asp
100 225      230      235      240
102 act cct acc acc ctt gcc agc cat agc acc aag act gat gcc agt agc      825
103 Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser
104      245      250      255
106 act cac cat agc acg gta cct cct ctc acc tcc tcc aat cac agc act      873
107 Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr
108      260      265      270
110 tct ccc cag ttg tct act ggg gtc tct ttc ttt ttc ctg tct ttt cac      921
111 Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His
112      275      280      285
114 att tca aac ctc cag ttt aat tcc tct ctg gaa gat ccc agc acc gac      969
115 Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
116      290      295      300
118 tac tac caa gag ctg cag aga gac att tct gaa atg ttt ttg cag att      1017
119 Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
120 305      310      315      320
122 tat aaa caa ggg ggt ttt ctg ggc ctc tcc aat att aag ttc agg cca      1065
123 Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
124      325      330      335
126 gga tct gtg gtg gta caa ttg act ctg gcc ttc cga gaa ggt acc atc      1113
127 Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile

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128          340          345          350
130 aat gtc cac gac gtg gag aca cag ttc aat cag tat aaa acg gaa gca      1161
131 Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
132          355          360          365
134 gcc tct cga tat aac ctg acg atc tca gac gtc agc gtg agt cat gtg      1209
135 Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser His Val
136          370          375          380
138 cca ttt cct ttc tct gcc cag tct ggg gct ggg gtg cca ggc tgg ggc      1257
139 Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly
140 385          390          395          400
142 atc gcg ctg ctg gtg ctg gtc tgt gtt ctg gtt gcg ctg gcc att gtc      1305
143 Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu Ala Ile Val
144          405          410          415
146 tat ctc att gcc ttg gct gtc tgt cag tgc cgc cga aag aac tac ggg      1353
147 Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly
148          420          425          430
150 cag ctg gac atc ttt cca gcc cgg gat acc tac cat cct atg agc gag      1401
151 Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu
152          435          440          445
154 tac ccc acc tac cac acc cat ggg cgc tat gtg ccc cct agc agt acc      1449
155 Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr
156          450          455          460
158 gat cgt agc ccc tat gag aag gtt tct gca ggt aat ggt ggc agc agc      1497
159 Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser
160 465          470          475          480
162 ctc tct tac aca aac cca gca gtg gca gcc act tct gcc aac ttg      1542
163 Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
164          485          490          495
166 taggggcacg tcgccctctg agctgagtgg      1572
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170 <211> LENGTH: 495
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 2
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177 1          5          10          15
180 Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
181          20          25          30
184 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
185          35          40          45
188 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
189          50          55          60
192 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
193 65          70          75          80
196 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
197          85          90          95
200 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
201          100          105          110
204 Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro

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205          115          120          125
208 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
209          130          135          140
212 Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His Gly Val Thr Ser
213 145          150          155          160
216 Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
217          165          170          175
220 Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala
221          180          185          190
224 Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser
225          195          200          205
228 Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr
229          210          215          220
232 Pro Ala Ser Lys Ser Thr Pro Pro Ser Ile Pro Ser His His Ser Asp
233 225          230          235          240
236 Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser
237          245          250          255
240 Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr
241          260          265          270
244 Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His
245          275          280          285
248 Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
249          290          295          300
252 Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
253 305          310          315          320
256 Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
257          325          330          335
260 Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile
261          340          345          350
264 Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
265          355          360          365
268 Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser His Val
269          370          375          380
272 Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly
273 385          390          395          400
276 Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu Ala Ile Val
277          405          410          415
280 Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly
281          420          425          430
284 Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu
285          435          440          445
288 Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr
289          450          455          460
292 Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser
293 465          470          475          480
296 Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
297          485          490          495
300 <210> SEQ ID NO: 3
301 <211> LENGTH: 9

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Input Set : A:\02-11-14 029395-017.ST25.txt

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302 <212> TYPE: PRT
303 <213> ORGANISM: Homo sapiens
305 <400> SEQUENCE: 3
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308 1 5
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312 <211> LENGTH: 9
313 <212> TYPE: PRT
314 <213> ORGANISM: Homo sapiens
316 <400> SEQUENCE: 4
318 Phe Leu Ser Phe His Ile Ser Asn Leu
319 1 5
322 <210> SEQ ID NO: 5
323 <211> LENGTH: 9
324 <212> TYPE: PRT
325 <213> ORGANISM: Homo sapiens
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330 1 5
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334 <211> LENGTH: 9
335 <212> TYPE: PRT
336 <213> ORGANISM: Homo sapiens
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341 1 5
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345 <211> LENGTH: 9
346 <212> TYPE: PRT
347 <213> ORGANISM: Homo sapiens
349 <400> SEQUENCE: 7
351 Ser Val Pro Val Thr Arg Pro Ala Leu
352 1 5
355 <210> SEQ ID NO: 8
356 <211> LENGTH: 9
357 <212> TYPE: PRT
358 <213> ORGANISM: Homo sapiens
360 <400> SEQUENCE: 8
362 Gly Val Pro Gly Trp Gly Ile Ala Leu
363 1 5
366 <210> SEQ ID NO: 9
367 <211> LENGTH: 9
368 <212> TYPE: PRT
369 <213> ORGANISM: Homo sapiens
371 <400> SEQUENCE: 9
373 Ala Pro Gly Ser Thr Ala Pro Pro Ala
374 1 5
377 <210> SEQ ID NO: 10
378 <211> LENGTH: 9

VERIFICATION SUMMARY

DATE: 04/30/2003

PATENT APPLICATION: US/09/658,621B

TIME: 13:04:23

Input Set : A:\02-11-14 029395-017.ST25.txt

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